

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: March 7, 2005, 06:56:21 ; Search time 22.0138 seconds  
(without alignments)  
1349.183 Million cell updates/sec

Title: US-09-939-537-35

Perfect score: 288  
Sequence: 1 PRASALPAPPTGSALPDPTQ.....VISFLGLGLGVACVLARTR 58

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284	98.6	240	1	CD7_HUMAN
2	96	33.3	762	2	09NGM7
3	85	29.5	359	2	082CF6
4	83.5	29.0	145	2	09VTE7
5	83	28.8	690	2	06PCS2
6	82	28.5	553	2	09VYF9
7	82	28.5	625	2	07ZC55
8	81.5	28.3	1149	2	013577
9	81	28.1	421	2	07KTK9
10	81	28.1	512	2	09VMI4
11	81	28.1	779	2	06TRP1
12	81	28.1	3326	2	07T591
13	80.5	28.0	763	2	09XDH2
14	80	27.8	169	2	07YXK4
15	80	27.8	421	2	098274
16	79.5	27.6	801	1	PRD4_HUMAN
17	78	27.1	210	2	07W2Q1
18	78	27.1	227	2	07W0K1
19	78	27.1	227	2	07WDP9
20	78	27.1	3388	2	07T5D9
21	77	26.7	375	2	093066
22	76.5	26.6	710	2	09CAL8
23	76	26.4	210	2	06I748
24	76	26.4	3084	2	08U211
25	75.5	26.2	329	2	06N737
26	75.5	26.2	798	2	09GZP2
27	75.5	26.2	1282	2	07Z836
28	75	26.0	237	2	06AC08
29	75	26.0	343	2	07PK73
30	75	26.0	378	2	066MN4
31	75	26.0	426	2	0742S1

32	75	26.0	518	2	Q8MQG8
33	75	26.0	524	2	002123
34	75	26.0	539	2	Q8MOG9
35	75	26.0	878	2	Q8L7M3
36	75	26.0	891	2	Q9ZM08
37	75	26.0	894	2	Q9FYB2
38	74.5	25.9	309	2	Q9PER1
39	74.5	25.9	554	2	Q8PUH9
40	74.5	25.9	759	2	Q6DW61
41	74.5	25.9	760	2	Q6DW64
42	74.5	25.9	762	1	FL15-CHICK
43	74.5	25.9	763	2	Q6DW62
44	74.5	25.9	764	2	Q6DW63
45	74.5	25.9	772	1	Z469_HUMAN

#### ALIGNMENTS

RESULT 1  
CD7\_HUMAN  
ID CD7\_HUMAN STANDARD; PRT; 240 AA.  
AC P05564;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE T-cell antigen CD7 precursor (GP40) (T-cell leukemia antigen) (TP41) (Leu-9).  
DE Name=CD7;  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8811517; PubMed=3501369;  
RA Aruffo A., Seed B.;  
RT "Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS  
cell expression system";  
RL EMBO J. 6:3313-3316(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9110576; PubMed=1703303;  
RA Schauberg R.L., Fleener D.B., Kurtzberg J., Haynes B.F., Kaufman R.E.;  
RT "Isolation and characterization of the genomic human CD7 gene:  
structural similarity with the murine Thy-1 gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:603-607(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klanner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkin R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Datschenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Umed T.B., Toshikiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richerson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fehy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP SEQUENCE OF 205-240 FROM N.A.

RA MEDLINE=91267564; PubMed=1711009;  
RA Yoshikawa K., Seto M., Ueda R., Obata Y., Norake K., Yokochi T.,  
RA Takahashi T.,  
RT "Molecular Cloning of the gene coding for the human T cell  
RT differentiation antigen CD7.";  
RL Immunogenetics 33:352-360(1991).  
RN [5]  
RP TOPOLOGY.  
RX MEDLINE=90063052; PubMed=2479685;  
RA Mare R.E., Searce R.M., Dietz M.A., Starmer C.F., Palmer T.J.,  
RA Haynes B.F.,  
RT "Characterization of the surface topography and putative tertiary  
RT structure of the human CD7 molecule.";  
RL J. Immunol. 143:3632-3640(1989).  
RN [6]  
RP INTERACTION WITH SECTM1.  
RX MEDLINE=20119303; PubMed=10652336; DOI=10.1074/jbc.275.5.3431;  
RA Lyman S.D., Escobar S., Rouseau A.-M., Armstrong A., Fanslow W.C.,  
RT "Identification of CD7 as a cognate of the human K12 (SECTM1)  
RT protein.";  
RL J. Biol. Chem. 275:3431-3437(2000).  
CC -1- FUNCTION: Not yet known.  
CC -1- SUBUNIT: Interacts with SECTM1.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD7 entry;  
WWW=http://www.ncbi.nlm.nih.gov/prow/cd/cd7.htm".  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
-----  
DR EMBL; X06180; CA29546.1; -;  
DR EMBL; M37271; AAA51953.1; -;  
DR EMBL; BC009293; AAH09293.1; -;  
DR EMBL; BC013297; AAH13297.1; -;  
DR EMBL; D00749; BAA00646.1; -;  
DR EMBL; D00747; BAA00646.1; JOINED.  
DR EMBL; D00748; BAA00646.1; JOINED.  
DR PIR; A39016; A39016.  
DR HSSP; P01607; 1BWW.  
DR Genew; HGNC:1695; CD7.  
DR H-invdb; HIX0014252; -.  
DR MIM; 186820; -;  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005624; C:membrane fraction; TAS.  
DR GO; GO:0005886; C:plasma membrane; TAS.  
DR GO; GO:0004872; F:receptor activity; TAS.  
DR GO; GO:0006955; P:immune response; TAS.  
DR GO; GO:0042110; P:T-cell activation; TAS.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; NAS.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Antigen; Glycoprotein; Immune response; Immunoglobulin domain;  
KW Lipoprotein; Palmitate; Receptor; Signal; T-cell;  
KW Transmembrane.  
KW  
FT SIGNAL 1 25  
FT CHAIN 26 240  
FT DOMAIN 26 180  
FT TRANSMEM 181 201  
FT DOMAIN 202 240  
FT DOMAIN 26 130  
FT DOMAIN 145 180  
FT  
FT DISULFID 35 142  
FT DISULFID 48 114

FT LIPID 198 198 S-palmitoyl cysteine.  
FT CARBOHYD 45 45 N-linked (GlcNAc...).  
FT CARBOHYD 96 96 N-linked (GlcNAc...).  
FT REPEAT 145 153 1.  
FT REPEAT 154 162 2.  
FT REPEAT 163 171 3.  
FT REPEAT 172 180 4.  
SQ SEQUENCE 240 AA; 25409 MW; EBBCE08279552108 CRC64;  
  
Query Match 98.6%; Score 284; DB 1; Length 240;  
Best Local Similarity 98.3%; Pred. No. 6.8e-17;  
Matches 57; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 PRASALPAPPTGSALPDPQTASALPDPAPASALPALAIYISFLGLGVAQVARTQ 58  
Db 147 PRASALPAPPTGSALPDPQTASALPDPAPASALPALAIYISFLGLGVAQVARTQ 204  
|||||  
  
RESULT 2  
Q9N9M7 PRELIMINARY; PRT; 762 AA.  
AC Q9N9M7;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein I3302.06.  
GN Name=I3302.06;  
OS Leishmania major.  
OC Eukaryota; Eukaryotes; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5664;  
RN [1] -  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RX MEDLINE=98146435; PubMed=9477341;  
RA Ivens A.C., Lewis S.M., Bagherzaden A., Zhang L., Chan H.M.,  
RA Smith D.F.,  
RT "A physical map of the Leishmania major Friedlin genome.";  
RL Genome Res. 8:135-145(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RA Hilbert H., Wedler H., Wedler E., Duesterhoeft A., Ivens A.C.,  
RA Quail M., Rajadream M.A., Barrell B.G.,  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL359781; CAB95309.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 762 AA; 79650 MW; C8AA1573FFD0F8F8 CRC64;  
  
Query Match 33.3%; Score 96; DB 2; Length 762;  
Best Local Similarity 39.0%; Pred. No. 2.5;  
Matches 16; Conservative 11; Mismatches 14; Indels 0; Gaps 0;  
  
Qy 1 PRASALPAPPTGSALPDPQTASALPDPAPASALPALAIYIS 41  
Db 378 PRASALPAPPTGSALPDPQTASALPDPAPASALPALAIYIS 418  
|||||  
  
RESULT 3  
Q82CF6 PRELIMINARY; PRT; 369 AA.  
AC Q82CF6;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=SAVS394;  
OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteriales; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomycetaceae; Streptomycetes.  
OX NCBI\_TaxID=33903;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680;

RA MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;  
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto O., Takahashi C.,  
 RA Shinoe M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,  
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,  
 RT "Genome sequence of an industrial microorganism Streptomyces  
 RT avermitilis: deducting the ability of producing secondary  
 RT metabolites.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MA-4680;  
 RX MEDLINE=22608306; PubMed=12692562;  
 RA Ikeda H., Ishikawa J., Hanamoto O., Shinoe M., Kikuchi H., Shiba T.,  
 RA Sakaki Y., Hattori M., Omura S.,  
 RT "Complete genome sequence and comparative analysis of the industrial  
 RT microorganism Streptomyces avermitilis.";  
 RL Nat. Biotechnol. 21:526-531(2003).  
 DR EMBL; AP005042; BAC73106.1;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR000620; DUF6.  
 DR Pfam; PF00892; DUF6; 2.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 369 AA; 36920 MW; 945D9B79E75AAE2 CRC64;  
 Query Match 29.5%; Score 85; DB 2; Length 369;  
 Best Local Similarity 47.2%; Pred. No. 12;  
 Matches 17; Conservative 6; Mismatches 13; Indels 0; Gaps 0;  
 Oy 1 PRASALPAPPTGALPDPTASALPDPPASALPAA 36  
 Db 316 PGAAVPGATATPATAVPATATPVTGATATPASA 351  
 RESULT 4  
 Q9VYE7 PRELIMINARY; PRT; 145 AA.  
 AC Q9VYE7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE CG12724-PA.  
 GN ORFNames=CG12724;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazer V.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fouts L., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,  
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Koditz C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon S., Nuskern D.R., Paclet J.M.,  
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Rainer K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,  
 RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri U.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs J.A., Myers R.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
 RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svitek R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
 RT melanogaster euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svitek R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.,  
 RT "The transposable elements of the Drosophila melanogaster euchromatin:  
 RT a genomics perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426059; PubMed=12537572;  
 RA Miura S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.B.,  
 RA Smith C.D., Tupy J.L., Whitfield E.D., Bayraktaroglu L., Berman B.P.,  
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.,  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 RN [15]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RL [6]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB003492; AAF48251.1; -.  
 DR FlyBase; FBgn0030470; CG12724.  
 SQ SEQUENCE 145 AA; 14524 MW; 12E97DA73AF8319 CRC64;  
 Query Match 29.0%; Score 83.5; DB 2; Length 145;  
 Best Local Similarity 44.1%; Pred. No. 6.8;  
 Matches 26; Conservative 5; Mismatches 21; Indels 7; Gaps 4;  
 Oy 4 SALPAPT--GSAALPDPTASALPDPPAS--ALPALAV--ISFLGLGAGVCVART 57  
 Db 33 SAATATPTASGSAATPTPTPT--PAPVAGGMLPPTLTGLGLGAGVCVSRLLRT 89  
 RESULT 5  
 Q6PCS2

```

ID 06PCS2 PRELIMINARY; PRT; 690 AA.
AC 06PCS2
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein zgc:64189.
GN ORFNames=zgc:64189;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Vellalton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pabby J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schmechel A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059189; AAH59189.1; -
DR ZFIN; ZDB-GENE-040426-1397; zgc:64189.
KM Hypothetical protein.
SQ SEQUENCE 690 AA; 7213 MW; 72E3F6955AFB95B2 CRC64;

Query Match 28.8%; Score 83; DB 2; Length 690;
Best Local Similarity 61.3%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 5 ALPAPPTGSALPDPQTASALPDPAPASALPAA 35
DB 358 ALPAPPTKIALPAPRLALPAPRLALPAA 388

RESULT 6
QYVF9 PRELIMINARY; PRT; 553 AA.
ID QYVF9;
AC QYVF9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE RE38286D.
GN ORFNames=CG12723;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

```

```

RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Munro J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celnik S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY119125; AAM50985.1; -
DR FlyBase; FBgn0010459; CG12723.
SQ SEQUENCE 553 AA; 58356 MW; 0FF2A5A1C6512B88 CRC64;

Query Match 28.5%; Score 82; DB 2; Length 553;
Best Local Similarity 41.7%; Pred. No. 30;
Matches 15; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 PRASALPAPPTGSALPDPQTASALPDPAPASALPAA 36
DB 348 PQAPAFISPPSVGVAVPTVPAPSPPTSGFPFPA 383

RESULT 7
ID Q722C5 PRELIMINARY; PRT; 625 AA.
AC Q722C5;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CG12723-PA.
GN ORFNames=CG12723;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostali M., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jaitani M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamor I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradlin A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodagel, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers R.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";

```

```

RL Science 287:2185-2195(2000).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacle J.W., Park S., Pfeiffer B.D., Richard S., Sodergren E.J.,
RA Svitek R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN (3)
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svitek R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN (4)
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettecous B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN (5)
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN (6)
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE004491; AAF48238.3; -.
DR Inctact: Q722C5; -.
DR FlyBase: FBgn0030459; CG12723.
SQ SEQUENCE 625 AA; 65250 MW; B82192937CB50E9D CRC64;

Query Match 28.5%; Score 82; DB 2; Length 625;
Best Local Similarity 41.7%; Pred. No. 33;
Matches 15; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

```

```

RA Whitney M.A., Grompe M., Friedberg A.S., Moses R.E.;
RT "Cloning and characterization of a human CDNA (INPL1) sharing
RT homology with inositol polyphosphate phosphatases."
RL Genomics 29:285-287(1995).
DR EMBL: L36818; AAA96658.1; -.
DR HSP: 043001; 1192.
DR GO: 0004437; F1:inositol or phosphatidylinositol phosphatase. .; NAS.
DR InterPro: IPR005135; Exo_endo_phos.
DR InterPro: IPR000300; IPPC.
DR Pfam: PF03372; Exo_endo_phos; 1.
DR SMART, SM00128; IPPC; 1.
SQ SEQUENCE 1149 AA; 126808 MW; DD3B54397362AA2F CRC64;

Query Match 28.3%; Score 81.5; DB 2; Length 1149;
Best Local Similarity 45.0%; Pred. No. 62;
Matches 27; Conservative 6; Mismatches 16; Indels 11; Gaps 5;

```

1 PRASALPA-PTG-SALPDQTASALPDPPASALPALAVIS--FLG-LGLGACV 53

Db 78 PRALAPPALPPTGSSPLPAPET----PTAASAPMGLSTVSHDYKSGYGLDLAV 133

```

RESULT 9
ID Q7KTK9 PRELIMINARY; PRT; 421 AA.
AC Q7KTK9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
GN CG5261-PA.
OR Names=CG5261;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gale R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabo G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Bailey D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitely A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McClintosh T.C., McLeod M.P., McPherson A.,
RA Merkulov G., Mhalhina N.V., Mobarry C., Morris J., Mosheret A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskeirn J.A., Pacle J.W.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheele F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

```

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celisner S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Paclel J.W., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Swistkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminke J.S., Bergman C.M., Krommiller B., Carlson J., Swistkas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celisner S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminke J.S., Millburn G.H., Prochnik S.B.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Betencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX Submittted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RG Submittted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RL -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.  
DR EMBL; AE003617; AAF52515.1; -.  
DR HSSP; P11961; 1B58.  
DR GO; GO:0045254; C:pyruvate dehydrogenase complex; IEA.  
DR GO; GO:0008415; F:acyltransferase activity; IEA.  
DR GO; GO:0004742; F:lipoyllysine-residue acetyltransferase. . ; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006096; F:glycolysis; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR001078; 2oxoacid\_dh.  
DR InterPro; IPR006257; Acetyltransferase.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR011053; Hybrid\_motif.  
DR InterPro; IPR003016; lipoyl\_BS.  
DR Pfam; PF00198; 2-oxoacid\_dh\_1.  
DR Pfam; PF00364; Biotin\_lipoyl\_1.  
DR ProDom; PD001115; 2oxoacid\_dh; 1.  
DR TIGRFAMs; TIGR01349; PDHac\_tif\_mito; 1.  
DR PROSITE; PS00189; LIPOLYL; 1.  
KW Acyltransferase; Lipoyl; Transferase.  
SQ SEQUENCE 421 AA; 44117 MW; A1P04AD0B0AC306 CRC64;

Query Match 28.1%; Score 81; DB 2; Length 421;  
Best Local Similarity 47.2%; Freq. No. 29;  
Matches 17; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

OY 3 ASALPAPPTGALPDPTASALPDPPAASALPALA 38  
| : | | | : | | | | : | | | | : | | | |  
DB 82 AAAAHPAHPAHPAHPAHPAHPAHPAHPAHPA 117  
RESULT 10  
ID 09VM14 PRELIMINARY; PRT; 512 AA.  
DT 01-MAY-2000 (TRENBLREL. 13, Created)  
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)  
DE CG5261-PB.  
GN ORFNames=CG5261;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champagne C.R., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abriil J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benes P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,  
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Keith K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.W., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Paclel J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheefel F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,  
RA Swistkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,  
RA Williams S.M., Woodardet, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celisner S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Paclel J.W., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Swistkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
 RA Patel S., Fried E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celinker S.E.;  
 RT "The transposable elements of the Drosophila melanogaster euchromatin:  
 RT a genomics perspective."  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RL [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Betencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter U., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 RT systematic review."  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX FlyBase;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
 CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.  
 DR EMBL; AE003617; AAF52514.1; -.  
 DR HSBP; P10515; 1FVC.  
 DR InAct; Q9VM14; -.  
 DR FlyBase; FBgn0031912; CGS261.  
 DR GO; GO:0045254; C:pyruvate dehydrogenase complex; IEA.  
 DR GO; GO:0008415; P:acyltransferase activity; IEA.  
 DR GO; GO:0004742; F:dihydrodipicolylsine-residue acetyltransferase...; IEA.  
 DR GO; GO:0005515; P:protein binding; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006096; P:glycolysis; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR001078; 2-oxoacid dh.  
 DR InterPro; IPR006257; AcetyltransferaseL.  
 DR InterPro; IPR000089; Biotin lipoyl.  
 DR InterPro; IPR004167; E3 binding.  
 DR InterPro; IPR011053; Hybrid motif.  
 DR InterPro; IPR003016; Lipoyl BS.  
 DR Pfam; PF00198; 2-oxoacid dh; 1.  
 DR Pfam; PF00364; Biotin lipoyl; 1.  
 DR Pfam; PF02817; E3 binding; 1.  
 DR ProDom; PD001115; 2-oxoacid dh; 1.  
 DR TIGRFAMs; TIGR01349; PDHac\_cif\_mito; 1.  
 DR PROSITE; PS00189; LIPOYL; 1.  
 KW Acyltransferase; Lipoyl; Transferase.  
 SQ SEQUENCE 512 AA; 54251 MW; AFA24470B56102FF CRC64;

Query Match 28.1%; Score 81; DB 2; Length 512;  
 Best Local Similarity 47.2%; Pred. No. 34;  
 Matches 17; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Oy 3 ASALPAPPTGSAIPDPTASALPDPAPALPATA 38  
 Db 173 AAAAPPAAPAPAPAPAPAPAPAPAPAPAPAAAA 208

RESULT 11  
 O6FTPI PRELIMINARY; PRT; 779 AA.  
 AC O6FTPI; 05-JUL-2004 (TREMblrel. 27, Created)  
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)  
 DE Similar to sp|P37370 Saccharomyces cerevisiae YLR337c VRP1.  
 GN ORFNames=CAGL0C009689;  
 OS Candida glabrata CBS138.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCB1\_TaxID=284593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CBS138;  
 RG Genolevures;  
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,  
 RA Goffard N., Fringault L., Aigle M., Anthonard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
 RA Bostrame A., Boyer J., Cattolico L., Confantlet F., de Daruvar A.,  
 RA Despons L., Fadre B., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerest A., Kozul R., Lemaire M., Loeur I., Ma L., Muller H.,  
 RA Nicaud J.M., Nikolski M., Oza S., Ozier-Kalogiropoulos O.,  
 RA Pellenz S., Pottier S., Richard G.F., Strub M.L., Suleau A.,  
 RA Sweeney D., Tekala P., Weslowski-Louvel M., Westhof E., Wirth B.,  
 RA Zeniou-Weyer M., Zivanovic I., Boleto-Pukhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.L.;  
 RT "Genome evolution in Yeasts."  
 RL Nature 430:35-44(2004)  
 DR EMBL; CR380953; CAG59330.1; -.  
 DR InterPro; IPR003124; WH2.  
 DR Pfam; PF02205; WH2; 2.  
 DR SMART; SM00246; WH2; 2.  
 SQ SEQUENCE 779 AA; 75743 MW; C850564FBFA3156B CRC64;

Query Match 28.1%; Score 81; DB 2; Length 779;  
 Best Local Similarity 51.2%; Pred. No. 49;  
 Matches 22; Conservative 2; Mismatches 17; Indels 2; Gaps 1;

Oy 1 PRASALPAPPTGSAIPDPTASALPDPAPALPATA 41  
 Db 406 PWASAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPALPATA 448

RESULT 12  
 O7T591 PRELIMINARY; PRT; 3326 AA.  
 AC O7T591;  
 DT 01-OCT-2003 (TREMblrel. 25, Created)  
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
 DE Large tegument protein.  
 GN Name=UL36;  
 OS Cercopithecine herpesvirus 1 (CeHV-1) (Simian herpes B virus).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCB1\_TaxID=10325;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22607624; PubMed=12721804;  
 RA Ohsawa K., Black D.H., Sato H., Rogers K., Eberle R.;  
 RT "Sequence and genetic arrangement of the UL region of the monkey B  
 RT virus (Cercopithecine herpesvirus 1) genome and comparison with the UL  
 RT region of other primate herpesviruses."  
 RL Arch. Virol. 148:989-997(2003).  
 DR EMBL; AB096160; BAC58076.2; -.  
 DR InterPro; IPR006928; Herpes teg N.  
 DR InterPro; IPR005210; Herpes teg N.  
 DR Pfam; PF04843; Herpes teg N; 1.  
 DR Pfam; PF03586; Herpes UL36; 1.  
 SQ SEQUENCE 3326 AA; 34556 MW; 6B53B3860F43CDP0 CRC64;

Query Match 28.1%; Score 81; DB 2; Length 3326;  
 Best Local Similarity 50.0%; Pred. No. 1,8e+02;  
 Matches 19; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

